GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 28, 2005, 18:44:48 ; Search time 191 Seconds
(without alignments)
30.124 Million cell updates/sec

Title: US-09-991-627-2
Perfect score: 50
Sequence: 1 NLEKETEGLR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	50	100.0	191	2	Q8HZ95	Q8hz95 pongo pygma
2	50	100.0	191	2	Q8HZ96	Q8hz96 gorilla gor
3	50	100.0	191	2	Q8HZ97	Q8hz97 pan troglod
4	50	100.0	249	2	Q6LDN9	Q6ldn9 homo sapien
5	50	100.0	249	2	AAA51747	Aaa51747 homo sapi
6	50	100.0	266	1	APA1_RABIT	P09809 oryctolagus
7	50	100.0	267	1	APA1_HUMAN	P02647 homo sapien
8	50	100.0	267	1	APA1_MACFA	P15568 macaca fasc
9	50	100.0	267	2	AAQ91811	Aaq91811 homo sapi
10	50	100.0	267	2	AAS68227	Aas68227 homo sapi
11	47	94.0	241	2	Q9TS49	Q9ts49 erinaceus e
12	44	88.0	265	1	APA1_PIG	P18648 sus scrofa
13	42	84.0	264	2	Q9Z2L4	Q9z2l4 mesocricetu
14	41	82.0	191	2	Q8HZ94	Q8hz94 saguinus oe
15	41	82.0	266	1	APA1_CANFA	P02648 canis famil
16	39	78.0	96	2	Q6NN75	Q6nn75 drosophila
17	39	78.0	96	2	AAR96210	Aar96210 drosophil
18	39	78.0	188	1	TFT1_PIG	O97557 sus scrofa
19	39	78.0	199	1	UBC4_DROME	P52486 drosophila
20	39	78.0	199	2	P91633	P91633 drosophila
21	39	78.0	259	1	APA1_RAT	P04639 rattus norv
22	39	78.0	390	1	TFT1_BOVIN	P27628 bos taurus
23	39	78.0	714	2	Q8PSU5	Q8psu5 methanosarc
24	38	76.0	56	2	O02762	O02762 ovis aries
25	38	76.0	142	2	Q85316	Q85316 rabbit fibr
26	38	76.0	190	2	Q9Q8N0	Q9q8n0 myxoma viru
27	38	76.0	190	2	Q9Q902	Q9q902 rabbit fibr
28	38	76.0	265	1	APA1_BOVIN	P15497 bos taurus
29	38	76.0	522	2	Q9N3E3	Q9n3e3 caenorhabdi
30	38	76.0	1734	2	Q7RBR3	Q7rbr3 plasmodium
31	38	76.0	1850	2	Q7R220	Q7r220 giardia lam
32	37	74.0	197	2	Q99LE1	Q99le1 mus musculu
33	37	74.0	978	1	RA50_AQUAE	O67124 aquifex aeo
34	36	72.0	79	2	Q6LD50	Q6ld50 mus sp. apo
35	36	72.0	79	2	AAB35539	Aab35539 mus sp. a
36	36	72.0	139	2	Q9FXP3	Q9fxp3 zinnia eleg
37	36	72.0	170	2	Q9FXP2	Q9fxp2 zinnia eleg
38	36	72.0	211	2	Q7VKD0	Q7vkd0 haemophilus
39	36	72.0	227	2	Q9SQK9	Q9sqk9 lycopersico
40	36	72.0	255	2	Q8LFD3	Q8lfd3 arabidopsis
41	36	72.0	263	2	O08855	O08855 mus musculu
42	36	72.0	263	2	O09042	O09042 mus musculu
43	36	72.0	264	1	APA1_MOUSE	Q00623 mus musculu
44	36	72.0	264	2	Q8BPD5	Q8bpd5 mus musculu
45	36	72.0	265	1	APA1_TUPGB	O18759 tupaia glis
46	36	72.0	274	2	Q8C089	Q8c089 mus musculu
47	36	72.0	282	2	Q9ZVG2	Q9zvg2 arabidopsis
48	36	72.0	288	2	Q8LC03	Q8lc03 arabidopsis
49	36	72.0	294	2	Q9S7A4	Q9s7a4 arabidopsis
50	36	72.0	301	2	Q43426	Q43426 daucus caro
51	36	72.0	304	2	Q6L4K0	Q614k0 solanum dem
52	36	72.0	304	2	AAT40488	Aat40488 solanum d
53	36	72.0	306	2	Q6L467	Q6l467 solanum dem
54	36	72.0	306	2	AAT40518	Aat40518 solanum d
55	36	72.0	308	2	Q43428	Q43428 daucus caro
56	36	72.0	313	2	Q6L452	Q6l452 solanum dem
57	36	72.0	313	2	AAT39931	Aat39931 solanum d
58	36	72.0	330	1	EXL2_MOUSE	Q9es89 mus musculu
59	36	72.0	330	2	Q8C197	Q8c197 mus musculu
60	36	72.0	348	2	Q98KF5	Q98kf5 rhizobium l
61	36	72.0	352	2	Q6F783	Q6f783 acinetobact
62	36	72.0	411	2	Q73R75	Q73r75 treponema d
63	36	72.0	411	2	AAS10713	Aas10713 treponema
64	36	72.0	463	2	Q6NIN9	Q6nin9 corynebacte
65	36	72.0	463	2	CAE49251	Cae49251 corynebac
66	36	72.0	1335	2	Q7V1N2	Q7v1n2 prochloroco
67	35	70.0	117	1	GVPK_HALME	Q02236 halobacteri
68	35	70.0	137	2	O27852	O27852 methanobact
69	35	70.0	180	2	Q9ETC6	Q9etc6 anabaena ci
70	35	70.0	180	2	Q9F970	Q9f970 anabaena sp
71	35	70.0	180	2	Q9F971	Q9f971 anabaena sp
72	35	70.0	180	2	Q9F972	Q9f972 aphanizomen
73	35	70.0	180	2	Q9F973	Q9f973 anabaena ap
74	35	70.0	180	2	Q9F974	Q9f974 anabaena fl
75	35	70.0	180	2	Q9F976	Q9f976 anabaena sp
76	35	70.0	180	2	Q9F977	Q9f977 anabaena so
77	35	70.0	180	2	Q9F978	Q9f978 anabaena ci
78	35	70.0	188	2	Q8WV38	Q8wv38 homo sapien
79	35	70.0	201	2	Q84Y37	Q84y37 thalictrum
80	35	70.0	203	2	Q9RG17	Q9rg17 anabaenopsi
81	35	70.0	203	2	Q9RG18	Q9rg18 anabaena ci
82	35	70.0	211	2	Q969X0	Q969x0 homo sapien
83	35	70.0	227	2	Q6TBM0	Q6tbm0 nodularia s
84	35	70.0	227	2	Q6TBM1	Q6tbm1 nodularia s
85	35	70.0	227	2	Q6TBM2	Q6tbm2 nostoc sp.
86	35	70.0	227	2	AAR92056	Aar92056 nostoc sp
87	35	70.0	227	2	AAR92057	Aar92057 nodularia
88	35	70.0	227	2	AAR92058	Aar92058 nodularia
89	35	70.0	234	1	NK4_HUMAN	P24001 homo sapien
90	35	70.0	234	2	Q96GK9	Q96gk9 homo sapien
91	35	70.0	273	2	Q7X4A0	Q7x4a0 tolypothrix
92	35	70.0	295	2	Q7X495	Q7x495 chlorogloeo
93	35	70.0	295	2	Q7X496	Q7x496 fischerella
94	35	70.0	295	2	Q7X498	Q7x498 nostoc ento
95	35	70.0	295	2	Q7X4A1	Q7x4a1 anabaena pl
96	35	70.0	295	2	Q8L134	Q8l134 nodularia s
97	35	70.0	295	2	Q8L135	Q8l135 fischerella
98	35	70.0	295	2	Q8L138	Q8l138 chlorogloeo
99	35	70.0	295	2	Q8L143	Q8l143 anabaenopsi
100	35	70.0	295	2	Q8L144	Q8l144 anabaena va
101	35	70.0	295	2	Q8L146	Q8l146 anabaena cy
102	35	70.0	295	2	Q8L147	Q8l147 nostoc linc
103	35	70.0	295	2	Q8L148	Q8l148 calothrix b
104	35	70.0	295	2	Q8L150	Q8l150 anabaena va

105	35	70.0	300	2	Q6NU65	Q6nu65 xenopus lae
106	35	70.0	300	2	AAH68735	Aah68735 xenopus l
107	35	70.0	318	2	Q8L998	Q8l998 arabidopsis
108	35	70.0	318	2	Q9LXR8	Q9lxr8 arabidopsis
109	35	70.0	334	2	Q8ERM3	Q8erm3 oceanobacil
110	35	70.0	338	2	Q8RD46	Q8rd46 thermoanaer
111	35	70.0	392	2	Q7WVB7	Q7wvb7 staphylococ
112	35	70.0	448	2	Q21178	Q21178 caenorhabdi
113	35	70.0	462	2	Q7U8T1	Q7u8t1 synechococc
114	35	70.0	486	2	Q8Q0A3	Q8q0a3 methanosarc
115	35	70.0	499	2	Q6ZE83	Q6ze83 synechocyst
116	35	70.0	499	2	BAD02017	Bad02017 synechocy
117	35	70.0	621	1	RPOC_NOSCO	P14563 nostoc comm
118	35	70.0	625	1	RPOC_ANASP	P22704 anabaena sp
119	35	70.0	657	2	O83140	O83140 treponema p
120	35	70.0	710	2	Q6IP90	Q6ip90 xenopus lae
121	35	70.0	710	2	AAH72027	Aah72027 xenopus l
122	35	70.0	862	2	Q6ZSE3	Q6zse3 homo sapien
123	35	70.0	862	2	BAC87010	Bac87010 homo sapi
124	35	70.0	988	2	Q6SLB1	Q6slb1 gibberella
125	35	70.0	988	2	AAR30127	Aar30127 gibberell
126	35	70.0	1092	2	Q7RR39	Q7rr39 plasmodium
127	35	70.0	1112	2	Q7US98	Q7us98 rhodopirell
128	35	70.0	1223	2	Q6FUN1	Q6fun1 candida gla
129	35	70.0	1310	2	Q949K0	Q949k0 lycopersico
130	35	70.0	1748	2	O57613	O57613 gallus gall
131	35	70.0	1780	2	Q6TV07	Q6tv07 homo sapien
132	35	70.0	1780	2	AAR25619	Aar25619 homo sapi
133	35	70.0	1840	2	Q90831	Q90831 gallus gall
134	35	70.0	2617	2	Q7R0Q0	Q7r0q0 giardia lam
135	34	68.0	55	2	Q6F9K2	Q6f9k2 acinetobact
136	34	68.0	114	1	Y467_BUCAI	P57539 buchnera ap
137	34	68.0	116	2	Q6JSY6	Q6jsy6 australobiu
138	34	68.0	116	2	AAQ77086	Aaq77086 australob
139	34	68.0	142	2	Q61384	Q61384 mus musculu
140	34	68.0	155	2	Q6CGB4	Q6cgb4 yarrowia li
141	34	68.0	182	2	Q9C4R0	Q9c4r0 methanococc
142	34	68.0	186	2	Q6LWP0	Q6lwp0 methanococc
143	34	68.0	186	2	CAF31225	Caf31225 methanoco
144	34	68.0	188	1	FLAC_METVO	O06636 methanococc
145	34	68.0	198	2	Q8BZ15	Q8bz15 mus musculu
146	34	68.0	205	2	Q6BVM3	Q6bvm3 debaryomyce
147	34	68.0	205	2	Q8DVW4	Q8dvw4 streptococc
148	34	68.0	222	1	BID2_YERPE	Q9agd4 yersinia pe
149	34	68.0	222	2	Q93AN8	Q93an8 yersinia ps
150	34	68.0	245	2	Q8ZX05	Q8zx05 pyrobaculum
151	34	68.0	254	1	MOAC_AQUAE	O66810 aquifex aeo
152	34	68.0	271	2	P89104	P89104 saccharomyc
153	34	68.0	291	2	Q93VD1	Q93vd1 oryza sativ
154	34	68.0	310	2	Q95Y78	Q95y78 caenorhabdi
155	34	68.0	328	2	Q6GPR0	Q6gpr0 xenopus lae
156	34	68.0	333	2	Q9BU49	Q9bu49 homo sapien
157	34	68.0	333	2	Q96D63	Q96d63 homo sapien
158	34	68.0	361	2	Q6BQU2	Q6bqu2 debaryomyce
159	34	68.0	375	2	Q947A1	Q947a1 prionitis l
160	34	68.0	378	2	Q8HYU6	Q8hyu6 oryctolagus
161	34	68.0	422	1	K1CW_HUMAN	Q9c075 homo sapien
162	34	68.0	422	1	K1CW_MOUSE	Q99ps0 mus musculu
163	34	68.0	422	2	Q8TC04	Q8tc04 homo sapien
164	34	68.0	422	2	Q6IFW4	Q6ifw4 rattus norv
165	34	68.0	422	2	Q8CB30	Q8cb30 mus musculu
166	34	68.0	422	2	BAC29649	Bac29649 mus muscu
167	34	68.0	436	2	Q6PJR2	Q6pjr2 homo sapien
168	34	68.0	436	2	AAH12734	Aah12734 homo sapi
169	34	68.0	466	2	Q6WIE1	Q6wie1 bacteriopha
170	34	68.0	466	2	AAQ64081	Aaq64081 bacteriop
171	34	68.0	497	2	Q8ZRZ7	Q8zrz7 salmonella
172	34	68.0	509	2	Q8FLC3	Q8flc3 escherichia
173	34	68.0	512	2	Q944K1	Q944k1 arabidopsis
174	34	68.0	514	2	Q8RWT8	Q8rwt8 arabidopsis
175	34	68.0	532	2	Q7V3T9	Q7v3t9 prochloroco
176	34	68.0	550	2	O70621	O70621 mus musculu
177	34	68.0	573	2	O65395	O65395 arabidopsis
178	34	68.0	589	2	Q6INL2	Q6inl2 xenopus lae
179	34	68.0	589	2	AAH72268	Aah72268 xenopus l
180	34	68.0	594	2	Q834D4	Q834d4 enterococcu
181	34	68.0	599	2	Q95SH3	Q95sh3 drosophila
182	34	68.0	621	2	Q7QQ03	Q7qq03 giardia lam
183	34	68.0	634	2	Q8CJ83	Q8cj83 rattus norv
184	34	68.0	637	2	Q8N825	Q8n825 homo sapien
185	34	68.0	651	2	Q8CJ84	Q8cj84 rattus norv
186	34	68.0	671	2	Q8CJ98	Q8cj98 rattus norv
187	34	68.0	678	2	Q8BRY9	Q8bry9 mus musculu
188	34	68.0	688	2	Q8CJ99	Q8cj99 rattus norv
189	34	68.0	728	2	Q8QZ68	Q8qz68 tomato mild
190	34	68.0	752	2	Q7VD86	Q7vd86 prochloroco
191	34	68.0	787	2	Q7QSY9	Q7qsy9 giardia lam
192	34	68.0	810	2	Q9U1A9	Q9u1a9 leishmania
193	34	68.0	924	2	Q6H4Y5	Q6h4y5 oryza sativ
194	34	68.0	959	2	Q8BY82	Q8by82 mus musculu
195	34	68.0	983	1	4ET_MOUSE	Q9est3 mus musculu
196	34	68.0	983	2	Q8CFW0	Q8cfw0 mus musculu
197	34	68.0	985	1	4ET_HUMAN	Q9nra8 homo sapien
198	34	68.0	985	2	CAG30272	Cag30272 homo sapi
199	34	68.0	1014	2	O35082	O35082 mus musculu
200	34	68.0	1014	2	O70175	O70175 mus musculu
201	34	68.0	1014	2	Q9Z2Y9	Q9z2y9 rattus norv
202	34	68.0	1037	2	Q7Q5D0	Q7q5d0 anopheles g
203	34	68.0	1112	2	Q8JTI3	Q8jti3 little cher
204	34	68.0	1178	2	Q84F12	Q84f12 cytophaga h
205	34	68.0	1195	1	YK76_YEAST	P36168 saccharomyc
206	34	68.0	1226	2	Q84VE4	Q84ve4 oryza sativ
207	34	68.0	1248	2	Q7XPJ0	Q7xpj0 oryza sativ
208	34	68.0	1290	1	SMC4_XENLA	P50532 xenopus lae
209	34	68.0	1467	2	Q8CHH8	Q8chh8 mus musculu
210	34	68.0	1528	2	Q991N1	Q991n1 little cher
211	34	68.0	1588	2	Q9ESK9	Q9esk9 mus musculu
212	34	68.0	1593	2	Q92601	Q92601 homo sapien
213	34	68.0	1594	2	Q8TDY2	Q8tdy2 homo sapien
214	34	68.0	1594	2	Q8WVU9	Q8wvu9 homo sapien
215	34	68.0	1627	2	Q7R264	Q7r264 giardia lam
216	34	68.0	1627	2	Q962Q0	Q962q0 giardia lam
217	34	68.0	1640	2	Q7T738	Q7t738 little cher
218	34	68.0	1980	2	Q991N2	Q991n2 little cher
219	34	68.0	1984	2	Q9VZ85	Q9vz85 drosophila
220	34	68.0	1984	2	Q8WQM0	Q8wqm0 drosophila
221	34	68.0	2033	1	EVPL_HUMAN	Q92817 homo sapien
222	34	68.0	2183	2	Q98589	Q98589 subacute sc
223	34	68.0	3102	2	O45614	O45614 caenorhabdi
224	33.5	67.0	522	2	Q73N94	Q73n94 treponema d
225	33.5	67.0	522	2	AAS11779	Aas11779 treponema
226	33	66.0	74	2	Q8HR55	Q8hr55 clivia gard
227	33	66.0	90	2	Q72TG2	Q72tg2 leptospira
228	33	66.0	90	2	Q8F1W2	Q8f1w2 leptospira
229	33	66.0	90	2	AAS69666	Aas69666 leptospir
230	33	66.0	92	2	Q6T6S6	Q6t6s6 bitis gabon
231	33	66.0	92	2	AAR25557	Aar25557 bitis gab
232	33	66.0	107	2	Q8T557	Q8t557 plasmodium
233	33	66.0	113	2	Q6BKC3	Q6bkc3 debaryomyce
234	33	66.0	156	2	Q9A3N8	Q9a3n8 caulobacter
235	33	66.0	161	2	Q8RC07	Q8rc07 thermoanaer
236	33	66.0	180	2	Q9F975	Q9f975 anabaena pe
237	33	66.0	183	1	TR13_HUMAN	Q15645 homo sapien
238	33	66.0	184	2	Q6DT75	Q6dt75 arabidopsis
239	33	66.0	203	1	RPOC_FISMU	P42074 fischerella
240	33	66.0	203	2	Q46580	Q46580 dermocarpa
241	33	66.0	203	2	Q9RG20	Q9rg20 cylindrospe
242	33	66.0	211	2	Q8H7A8	Q8h7a8 arabidopsis
243	33	66.0	213	2	Q9ZDE0	Q9zde0 rickettsia
244	33	66.0	226	2	Q7P7J6	Q7p7j6 fusobacteri
245	33	66.0	226	2	Q8RFI0	Q8rfi0 fusobacteri
246	33	66.0	227	2	Q6TBL8	Q6tbl8 microcystis
247	33	66.0	227	2	Q6TBL9	Q6tbl9 microcystis
248	33	66.0	227	2	Q6TBM3	Q6tbm3 anabaena ci
249	33	66.0	227	2	Q6TBM4	Q6tbm4 anabaena sp
250	33	66.0	227	2	AAR92054	Aar92054 anabaena

OM protein - protein search, using sw model

Run on: January 28, 2005, 18:43:43 ; Search time 154 Seconds
(without alignments)
23.294 Million cell updates/sec

Title: US-09-991-627-2
Perfect score: 50
Sequence: 1 NLEKETEGLR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	50	100.0	10	7	ADD94064	Add94064 Human apo
2	50	100.0	16	4	AAG62607	Aag62607 Apolipopr
3	50	100.0	119	4	AAU30468	Aau30468 Novel hum
4	50	100.0	120	4	AAU30469	Aau30469 Novel hum
5	50	100.0	120	4	AAU30267	Aau30267 Novel hum
6	50	100.0	160	6	ABP75964	Abp75964 Human GEN
7	50	100.0	166	4	AAU28372	Aau28372 Novel hum
8	50	100.0	168	5	AAE24649	Aae24649 Human MSP
9	50	100.0	168	5	AAE24648	Aae24648 Human MSP
10	50	100.0	170	6	ADA61215	Ada61215 Human 18K
11	50	100.0	201	5	AAE24644	Aae24644 Human non
12	50	100.0	201	5	AAE24650	Aae24650 Human MSP
13	50	100.0	201	5	AAE24651	Aae24651 Human MSP
14	50	100.0	207	5	ABP53596	Abp53596 Human NOV
15	50	100.0	211	5	ABG69598	Abg69598 Human NOV
16	50	100.0	211	7	ADJ83023	Adj83023 Human NOV
17	50	100.0	212	5	AAE24643	Aae24643 Human his
18	50	100.0	221	4	AAU29835	Aau29835 Novel hum
19	50	100.0	240	5	ABP53595	Abp53595 Human NOV
20	50	100.0	240	5	ABG69597	Abg69597 Human NOV
21	50	100.0	240	7	ADJ83021	Adj83021 Human NOV
22	50	100.0	243	1	AAP81082	Aap81082 Sequence
23	50	100.0	243	5	AAE24653	Aae24653 Human apo
24	50	100.0	243	5	ABG97579	Abg97579 Human apo
25	50	100.0	243	7	ADD29960	Add29960 Mutant ma
26	50	100.0	243	8	ADO06580	Ado06580 Apolipopr
27	50	100.0	244	4	AAU28184	Aau28184 Novel hum
28	50	100.0	244	5	ABG97580	Abg97580 Human apo
29	50	100.0	249	7	ADJ83085	Adj83085 Human pro
30	50	100.0	250	5	AAE24642	Aae24642 Human Pro
31	50	100.0	252	6	ABR43302	Abr43302 Human lip
32	50	100.0	254	7	ADD29962	Add29962 Mature hu
33	50	100.0	254	7	ADD29961	Add29961 Mutant ma
34	50	100.0	258	5	ABG97582	Abg97582 Human apo
35	50	100.0	261	5	ABG97598	Abg97598 Human apo
36	50	100.0	264	2	AAR56864	Aar56864 Apo-lipop
37	50	100.0	264	2	AAR56863	Aar56863 Apo-lipop
38	50	100.0	267	1	AAP61079	Aap61079 Assumed h
39	50	100.0	267	1	AAP82128	Aap82128 Entire hu
40	50	100.0	267	2	AAR72705	Aar72705 Human apo
41	50	100.0	267	2	AAR34032	Aar34032 Sequence
42	50	100.0	267	2	AAW08602	Aaw08602 Human apo
43	50	100.0	267	2	AAY18675	Aay18675 Human apo
44	50	100.0	267	4	AAB47620	Aab47620 Full leng
45	50	100.0	267	5	AAO15892	Aao15892 Human apo
46	50	100.0	267	5	ABG97593	Abg97593 Human apo
47	50	100.0	267	6	ABR44031	Abr44031 Human apo
48	50	100.0	267	6	ABR44032	Abr44032 Human mut
49	50	100.0	267	6	ABP57065	Abp57065 Human apo
50	50	100.0	267	6	ADA61214	Ada61214 Human apo
51	50	100.0	267	7	ADJ68447	Adj68447 Human hea
52	50	100.0	267	7	ADJ83084	Adj83084 Human apo
53	50	100.0	267	7	ADJ83086	Adj83086 Apolipopr
54	50	100.0	267	7	ADJ83087	Adj83087 Crab-eati
55	50	100.0	267	7	ADJ83083	Adj83083 Human pro
56	50	100.0	267	8	ADE76862	Ade76862 Human pro
57	50	100.0	267	8	ADI19752	Adi19752 Human APO
58	50	100.0	268	1	AAP80668	Aap80668 Recombina
59	50	100.0	273	5	ABG97597	Abg97597 Human apo
60	50	100.0	275	6	AAO30162	Aao30162 Human APO
61	50	100.0	299	4	AAU33170	Aau33170 Novel hum
62	50	100.0	301	5	ABG97583	Abg97583 Human apo
63	50	100.0	301	5	ABG97581	Abg97581 Human apo
64	50	100.0	304	5	ABG97584	Abg97584 Human apo
65	50	100.0	304	5	ABG97586	Abg97586 Human apo
66	50	100.0	304	5	ABG97585	Abg97585 Human apo
67	50	100.0	306	5	ABG97588	Abg97588 Human apo
68	50	100.0	306	5	ABG97587	Abg97587 Human apo
69	50	100.0	306	5	ABG97589	Abg97589 Human apo
70	50	100.0	316	5	ABG97599	Abg97599 Human apo
71	50	100.0	316	5	ABG97596	Abg97596 Human apo
72	50	100.0	323	5	ABG97602	Abg97602 Human apo
73	50	100.0	323	5	ABG97601	Abg97601 Human apo
74	50	100.0	323	5	ABG97600	Abg97600 Human apo
75	50	100.0	325	5	ABG97603	Abg97603 Human apo
76	50	100.0	325	5	ABG97604	Abg97604 Human apo
77	50	100.0	325	5	ABG97605	Abg97605 Human apo
78	50	100.0	329	5	ABG97592	Abg97592 Human apo
79	50	100.0	336	5	ABG97594	Abg97594 Human apo
80	50	100.0	337	5	ABG97595	Abg97595 Human apo
81	50	100.0	344	5	ABG97606	Abg97606 Human apo
82	50	100.0	392	5	AAE24652	Aae24652 Human MSP
83	50	100.0	414	5	AAE24646	Aae24646 Human MSP
84	50	100.0	422	5	AAE24647	Aae24647 Human MSP
85	47	94.0	151	4	AAO02278	Aao02278 Human pol
86	47	94.0	180	8	ADJ93927	Adj93927 Western E
87	46	92.0	318	4	AAU30268	Aau30268 Novel hum
88	42	84.0	154	4	AAO12095	Aao12095 Human pol
89	39	78.0	199	4	ABB63741	Abb63741 Drosophil
90	39	78.0	259	7	ADF30722	Adf30722 Rat angio
91	39	78.0	259	7	ADF30714	Adf30714 Rat angio
92	39	78.0	259	7	ADF30724	Adf30724 Rat angio
93	39	78.0	259	7	ADF30726	Adf30726 Rat angio
94	36	72.0	201	3	AAG21619	Aag21619 Arabidops
95	36	72.0	212	3	AAG21618	Aag21618 Arabidops
96	36	72.0	255	3	AAG21617	Aag21617 Arabidops
97	36	72.0	280	3	AAG08396	Aag08396 Arabidops
98	36	72.0	288	3	AAG08395	Aag08395 Arabidops

99	36	72.0	294	3	AAG08394	Aag08394	Arabidops
100	36	72.0	428	6	ABU26010	Abu26010	Protein e
101	35	70.0	47	4	AAO12396	Aao12396	Human pol
102	35	70.0	100	3	AAG00952	Aag00952	Human sec
103	35	70.0	130	5	ADK35406	Adk35406	Novel hum
104	35	70.0	137	4	AAM25867	Aam25867	Human pro
105	35	70.0	138	6	ABP76299	Abp76299	Human GEN
106	35	70.0	139	6	ABR69617	Abr69617	Human CGD
107	35	70.0	139	6	ABR69656	Abr69656	Human CGD
108	35	70.0	139	7	ADE28190	Ade28190	Human MDD
109	35	70.0	139	7	ADE28182	Ade28182	Human MDD
110	35	70.0	168	6	ABR69655	Abr69655	Human CGD
111	35	70.0	177	4	AAM81943	Aam81943	Human hae
112	35	70.0	188	5	ABP64799	Abp64799	Human pro
113	35	70.0	188	6	ABR48482	Abr48482	Human Nat
114	35	70.0	188	7	ADG10828	Adg10828	Human STA
115	35	70.0	188	7	ADG10830	Adg10830	Human STA
116	35	70.0	188	8	ADG20487	Adg20487	Human NK4
117	35	70.0	194	4	AAM81880	Aam81880	Human hae
118	35	70.0	211	6	ADA55287	Ada55287	Human pro
119	35	70.0	211	6	ABU00128	Abu00128	Human nov
120	35	70.0	222	6	ABR58508	Abr58508	Human sec
121	35	70.0	234	6	ABR92129	Abr92129	Human cer
122	35	70.0	234	6	ABR92128	Abr92128	Human cer
123	35	70.0	234	7	ADG10720	Adg10720	Human STA
124	35	70.0	234	7	ADG10832	Adg10832	Human STA
125	35	70.0	234	7	ADN95584	Adn95584	Human BEC
126	35	70.0	234	8	ADJ75301	Adj75301	Marker ge
127	35	70.0	245	7	ADJ68279	Adj68279	Human hea
128	35	70.0	245	7	ADJ68280	Adj68280	Human hea
129	35	70.0	259	3	AAG04623	Aag04623	Arabidops
130	35	70.0	287	3	AAG04622	Aag04622	Arabidops
131	35	70.0	318	3	AAG04621	Aag04621	Arabidops
132	35	70.0	376	7	ADF06455	Adf06455	Bacterial
133	35	70.0	657	6	ABU48469	Abu48469	Protein e
134	35	70.0	1102	4	ABG29358	Abg29358	Novel hum
135	35	70.0	1102	8	ADJ57489	Adj57489	Human pol
136	35	70.0	1342	8	ADJ57463	Adj57463	Breast ca
137	35	70.0	1456	4	ABG29357	Abg29357	Novel hum
138	35	70.0	1456	8	ADJ57490	Adj57490	Human pol
139	34	68.0	67	5	ABP04319	Abp04319	Human ORF
140	34	68.0	78	4	AAU22150	Aau22150	Human car
141	34	68.0	78	7	ADE46118	Ade46118	Human car
142	34	68.0	80	4	AAM92940	Aam92940	Human dig
143	34	68.0	80	4	AAU20036	Aau20036	Human liv
144	34	68.0	80	5	ABP40897	Abp40897	Human liv
145	34	68.0	80	7	ADJ15015	Adj15015	Human liv
146	34	68.0	96	4	AAM92666	Aam92666	Human dig
147	34	68.0	96	4	AAU22660	Aau22660	Novel hum
148	34	68.0	96	7	ADB32500	Adb32500	Human nov
149	34	68.0	113	5	ABG93329	Abg93329	C. albica
150	34	68.0	123	5	ABP08632	Abp08632	Human ORF
151	34	68.0	143	4	ADM20065	Adm20065	Protein e
152	34	68.0	175	6	ABU29509	Abu29509	Protein e
153	34	68.0	179	4	AAO00017	Aao00017	Human pol
154	34	68.0	197	7	ADC94507	Adc94507	E. faeciu
155	34	68.0	225	7	ABM73793	Abm73793	DNA clone
156	34	68.0	234	4	ABG14913	Abg14913	Novel hum
157	34	68.0	237	4	AAB63635	Aab63635	Human gas
158	34	68.0	271	6	ABR53465	Abr53465	Protein s
159	34	68.0	271	7	ADK64594	Adk64594	Disease t
160	34	68.0	275	7	ADE96050	Ade96050	Human uri
161	34	68.0	336	7	ADE96049	Ade96049	Human uri
162	34	68.0	422	3	AAY52399	Aay52399	Human ker
163	34	68.0	422	4	AAB93570	Aab93570	Human pro
164	34	68.0	422	5	ABG96336	Abg96336	Human ova
165	34	68.0	422	5	AAE20424	Aae20424	Human ker
166	34	68.0	422	5	ABP54685	Abp54685	Metastati
167	34	68.0	422	7	ABM78946	Abm78946	Breast ca
168	34	68.0	422	8	ADJ75461	Adj75461	Marker ge
169	34	68.0	422	8	ADJ76249	Adj76249	Marker ge
170	34	68.0	422	8	ADJ75484	Adj75484	Marker ge
171	34	68.0	422	8	ADJ76236	Adj76236	Marker ge
172	34	68.0	430	7	ADE96057	Ade96057	Human uri
173	34	68.0	466	3	AAB43921	Aab43921	Human can
174	34	68.0	466	4	AAB63634	Aab63634	Human gas
175	34	68.0	475	7	ADC94239	Adc94239	E. faeciu
176	34	68.0	492	4	ABB52501	Abb52501	Escherich
177	34	68.0	497	6	ABU47012	Abu47012	Protein e
178	34	68.0	507	7	ADE96048	Ade96048	Human uri
179	34	68.0	519	6	ABR40118	Abr40118	Human cel
180	34	68.0	550	2	AAW63674	Aaw63674	Polypepti
181	34	68.0	550	4	AAB73617	Aab73617	Mouse Klo
182	34	68.0	560	4	ABB47265	Abb47265	Enterococ
183	34	68.0	596	7	ADH86631	Adh86631	Enterococ
184	34	68.0	607	7	ADE96052	Ade96052	Human uri
185	34	68.0	637	7	ADM05658	Adm05658	Human pro
186	34	68.0	663	7	ADE96047	Ade96047	Human uri
187	34	68.0	670	4	ABG12544	Abg12544	Novel hum
188	34	68.0	821	4	ABG14530	Abg14530	Novel hum
189	34	68.0	821	4	ABG07875	Abg07875	Novel hum
190	34	68.0	874	4	ABG10246	Abg10246	Novel hum
191	34	68.0	932	7	ADE96044	Ade96044	Human uri
192	34	68.0	964	7	ADE96056	Ade96056	Human uri
193	34	68.0	967	6	ABR41060	Abr41060	Human MAP
194	34	68.0	968	7	ADC31834	Adc31834	Human nov
195	34	68.0	985	7	ADE96040	Ade96040	Human uri
196	34	68.0	985	7	ADE96041	Ade96041	Human uri
197	34	68.0	985	7	ADJ70429	Adj70429	Human hea
198	34	68.0	986	7	ADC31833	Adc31833	Human nov
199	34	68.0	1009	7	ADE96051	Ade96051	Human uri
200	34	68.0	1014	2	AAW63673	Aaw63673	Polypepti
201	34	68.0	1014	4	AAB73616	Aab73616	Mouse Klo
202	34	68.0	1195	7	ADK64212	Adk64212	Disease t
203	34	68.0	1234	4	ABB68510	Abb68510	Drosophil
204	34	68.0	1588	8	ADH14288	Adh14288	Mouse ret
205	34	68.0	1591	6	ABR41061	Abr41061	Human MAP
206	34	68.0	1594	8	ADH14287	Adh14287	Human ret
207	34	68.0	1644	4	ABG12176	Abg12176	Novel hum
208	34	68.0	2033	7	ADJ68613	Adj68613	Human hea
209	34	68.0	2033	8	ADJ75622	Adj75622	Marker ge
210	33	66.0	45	8	ABO56509	Abo56509	Human gen
211	33	66.0	114	2	AAY76562	Aay76562	Human ova
212	33	66.0	138	4	AAM42205	Aam42205	Human pol
213	33	66.0	148	2	AAW28082	Aaw28082	Staphyloc
214	33	66.0	159	4	AAU33520	Aau33520	Enterococ
215	33	66.0	194	2	AAR53552	Aar53552	Thyroid h
216	33	66.0	194	2	AAW85110	Aaw85110	Thyroid h
217	33	66.0	194	2	AAW92398	Aaw92398	Human TR-
218	33	66.0	194	2	AAY40591	Aay40591	Partial a
219	33	66.0	228	4	AAU33878	Aau33878	Staphyloc
220	33	66.0	230	6	ABU43725	Abu43725	Protein e
221	33	66.0	230	6	ABU43263	Abu43263	Protein e
222	33	66.0	231	4	AAU36696	Aau36696	Staphyloc
223	33	66.0	231	6	ABU16228	Abu16228	Protein e
224	33	66.0	231	6	ABM71195	Abm71195	Staphyloc
225	33	66.0	233	5	ABB49740	Abb49740	Listeria
226	33	66.0	233	6	ABU32874	Abu32874	Protein e
227	33	66.0	235	5	ABP40300	Abp40300	Staphyloc
228	33	66.0	239	6	ABU29773	Abu29773	Protein e
229	33	66.0	240	4	AAM38766	Aam38766	Human pol
230	33	66.0	240	5	ABB75727	Abb75727	Human RNA
231	33	66.0	240	6	ABU25456	Abu25456	Protein e
232	33	66.0	241	3	AAG41492	Aag41492	Arabidops
233	33	66.0	244	3	AAG41491	Aag41491	Arabidops
234	33	66.0	244	6	ABU14527	Abu14527	Protein e
235	33	66.0	249	4	ABG09036	Abg09036	Novel hum
236	33	66.0	249	7	ADC94893	Adc94893	E. faeciu
237	33	66.0	257	4	AAU35088	Aau35088	Enterococ
238	33	66.0	262	4	AAM40552	Aam40552	Human pol
239	33	66.0	298	7	ADB65418	Adb65418	Human pro
240	33	66.0	299	4	AAB95448	Aab95448	Human pro
241	33	66.0	299	4	AAM94031	Aam94031	Human sto
242	33	66.0	323	3	AAG41490	Aag41490	Arabidops
243	33	66.0	365	4	AAM93464	Aam93464	Human pol
244	33	66.0	365	4	AAM40421	Aam40421	Human pol

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 28, 2005, 18:55:58 ; Search time 40 Seconds
(without alignments)
24.054 Million cell updates/sec

Title: US-09-991-627-2
Perfect score: 50
Sequence: 1 NLEKETEGLR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	50	100.0	241	2	A24998	apolipoprotein A-I
2	50	100.0	265	1	LPRB1B	apolipoprotein A-I
3	50	100.0	266	1	LPRB1Z	apolipoprotein A-I
4	50	100.0	267	1	A26529	apolipoprotein A-I
5	50	100.0	267	1	LPHUA1	apolipoprotein A-I
6	50	100.0	267	2	JS0079	apolipoprotein A-I
7	44	88.0	231	2	JQ0704	apolipoprotein A-I
8	44	88.0	264	2	S31394	apolipoprotein A-I
9	44	88.0	265	2	A46018	apolipoprotein AI
10	41	82.0	266	1	LPDGA1	apolipoprotein A-I
11	39	78.0	199	2	T08465	ubiquitin-protein
12	39	78.0	259	2	A24700	apolipoprotein A-I
13	39	78.0	389	2	A40809	enamelin, 44K - bo
14	38	76.0	265	2	JT0672	apolipoprotein A-I
15	38	76.0	265	2	A56858	apolipoprotein A-I
16	37	74.0	978	2	A70387	conserved hypothet
17	36	72.0	262	2	JC1237	apolipoprotein A-I
18	36	72.0	264	2	S22420	apolipoprotein A-I
19	36	72.0	282	2	F86396	hypothetical prote
20	36	72.0	294	2	H96719	homeobox gene 13 p
21	36	72.0	301	2	T14331	homeotic protein -
22	35	70.0	117	2	S28124	gas-vesicle operon
23	35	70.0	137	2	H69110	hypothetical prote
24	35	70.0	234	2	I56140	NK and T lymphocyt
25	35	70.0	318	2	T49167	hypothetical prote
26	35	70.0	448	2	T23263	hypothetical prote
27	35	70.0	621	2	A32838	DNA-directed RNA p
28	35	70.0	625	2	B42361	DNA-directed RNA p
29	35	70.0	625	2	AE2005	RNA polymerase gam
30	35	70.0	657	2	B71367	probable rep helic
31	35	70.0	1606	2	T34073	paranemin - chicke
32	35	70.0	1840	2	T29091	transitin - chicke
33	34	68.0	114	2	D84984	hypothetical prote
34	34	68.0	142	2	I48282	gene CC1 protein -
35	34	68.0	188	2	T44948	flagella-related p
36	34	68.0	222	2	AE0276	dethiobiotin synth
37	34	68.0	254	2	F70347	molybdenum cofacto
38	34	68.0	573	2	A86253	hypothetical prote
39	34	68.0	1014	2	JE0333	klotho protein - r
40	34	68.0	1195	2	S38174	probable purine nu
41	34	68.0	1290	2	A55094	chromosomal protei
42	34	68.0	2823	2	F87908	protein T22A3.8 [i
43	34	68.0	2823	2	T23064	hypothetical prote
44	34	68.0	3102	2	T43291	laminin alpha chai
45	33	66.0	156	2	B87641	transcription regu
46	33	66.0	213	2	F71696	hypothetical prote
47	33	66.0	231	2	E89960	hypothetical prote
48	33	66.0	233	2	AF1367	16S pseudouridylat
49	33	66.0	233	2	AG1736	16S pseudouridylat
50	33	66.0	250	2	F83474	hypothetical prote
51	33	66.0	397	2	C72354	conserved hypothet
52	33	66.0	405	2	AF2735	DNA-damage inducib
53	33	66.0	407	2	A97149	molybdopterin bios
54	33	66.0	424	2	JC5891	omega 6 desaturase
55	33	66.0	434	2	T32520	hypothetical prote
56	33	66.0	437	2	F97516	DNA damage inducib
57	33	66.0	438	2	T33601	hypothetical prote
58	33	66.0	464	2	E83834	flagellin BH1477 [
59	33	66.0	509	2	A43580	coccolysin (EC 3.4
60	33	66.0	939	2	T32521	hypothetical prote
61	33	66.0	1381	1	S45781	probable calcium-b
62	33	66.0	1474	2	T18281	hypothetical prote
63	32	64.0	133	2	JE0311	serine proteinase
64	32	64.0	144	1	TVVPBD	small T antigen -
65	32	64.0	211	1	ZKBPT4	transcription regu
66	32	64.0	248	2	T33230	hypothetical prote
67	32	64.0	263	2	E86215	protein T6D22.16 [
68	32	64.0	309	2	B96602	hypothetical prote
69	32	64.0	320	2	G84676	hypothetical prote
70	32	64.0	360	2	T32519	hypothetical prote
71	32	64.0	372	2	T24891	hypothetical prote
72	32	64.0	379	2	AD1974	thiamin-phosphate
73	32	64.0	380	2	A42832	factor VIII-associ
74	32	64.0	384	2	T24075	hypothetical prote
75	32	64.0	396	1	XNECD	aspartate transami
76	32	64.0	396	2	AD0616	aspartate aminotra
77	32	64.0	396	2	A85619	aspartate aminotra
78	32	64.0	396	2	C90755	aspartate aminotra
79	32	64.0	413	2	T43810	methylaspartate am
80	32	64.0	413	2	A85575	probable methylasp
81	32	64.0	413	2	A99724	3-methylaspartate
82	32	64.0	424	2	C82516	type I restriction
83	32	64.0	430	2	A87708	hypothetical prote
84	32	64.0	438	2	T52082	alpha galactosyltr
85	32	64.0	475	1	WMADP6	early E1B 53K prot
86	32	64.0	489	1	S66088	conserved hypothet
87	32	64.0	554	1	TVVPBF	large T antigen -
88	32	64.0	575	2	C83313	probable type II s
89	32	64.0	596	2	T17333	hypothetical prote
90	32	64.0	607	2	H90590	hypothetical prote
91	32	64.0	609	2	S55270	catrocollastatin p
92	32	64.0	678	2	S44925	IB3/5-polypeptide
93	32	64.0	792	2	F83304	probable restricti
94	32	64.0	793	2	E64545	hypothetical prote
95	32	64.0	817	2	T03852	protein phosphatas
96	32	64.0	873	2	T05189	glutamyl aminopept
97	32	64.0	902	2	S33918	dynamin-like prote
98	32	64.0	916	2	F71962	hypothetical prote
99	32	64.0	932	2	S65214	probable alpha/gam
100	32	64.0	976	2	D96714	DNA-directed RNA p
101	32	64.0	980	2	E86589	CT590 hypothetical
102	32	64.0	980	2	E72035	conserved hypothet

103	32	64.0	992	2	T46337	hypothetical prote
104	32	64.0	1073	2	S69079	hypothetical prote
105	32	64.0	1277	2	T15109	hypothetical prote
106	32	64.0	1396	2	F87311	DNA-directed RNA p
107	32	64.0	1532	2	H96795	hypothetical prote
108	32	64.0	2254	2	D86215	protein T6D22.14 [
109	32	64.0	2677	2	A38194	desmoplakin I - hu
110	32	64.0	4151	2	T13734	groovin gene prote
111	31	62.0	99	2	B46598	ski-related protei
112	31	62.0	101	2	A46598	transforming prote
113	31	62.0	116	2	H90133	40S ribosomal prot
114	31	62.0	125	2	T05633	hypothetical prote
115	31	62.0	141	2	F64411	hypothetical prote
116	31	62.0	157	2	T24917	hypothetical prote
117	31	62.0	181	1	Z4BPT9	ribonucleoside-tri
118	31	62.0	190	2	T23702	hypothetical prote
119	31	62.0	209	2	S32681	DNA-directed RNA p
120	31	62.0	223	2	AB1541	ABC transporters,
121	31	62.0	224	2	AD1407	ribulose-5-phospha
122	31	62.0	224	2	AD1783	ribulose-5-phospha
123	31	62.0	235	2	H72025	probable pseudouri
124	31	62.0	235	2	F86598	pseudouridine synt
125	31	62.0	235	2	G81515	ribosomal large ch
126	31	62.0	238	2	B72320	ribonuclease HII -
127	31	62.0	241	2	E81741	ribosomal large ch
128	31	62.0	241	2	F71478	probable pseudouri
129	31	62.0	261	2	T16732	hypothetical prote
130	31	62.0	273	2	H86904	hypothetical prote
131	31	62.0	286	1	D64775	acyl-CoA thioleste
132	31	62.0	286	2	A37053	flagellar filament
133	31	62.0	286	2	AD0560	acyl-CoA thioester
134	31	62.0	286	2	F85542	acyl-CoA thioester
135	31	62.0	286	2	B90692	acyl-CoA thioester
136	31	62.0	286	2	S07533	puff II/9A-2 prote
137	31	62.0	287	2	A27082	2,4-dichlorophenox
138	31	62.0	288	1	S42566	protein kinase (EC
139	31	62.0	300	2	A81418	pseudouridylate sy
140	31	62.0	303	2	F71680	hypothetical prote
141	31	62.0	304	1	FLBS68	flagellin (hag) -
142	31	62.0	304	2	D72316	ribosomal large su
143	31	62.0	305	2	T09370	shikimate kinase h
144	31	62.0	321	2	G64463	hypothetical prote
145	31	62.0	350	2	C97276	mannose-1-phosphat
146	31	62.0	353	2	F84252	phycocyanin alpha
147	31	62.0	354	2	C90173	3-dehydroquinate s
148	31	62.0	374	2	D81937	probable ribosomal
149	31	62.0	374	2	A81168	ribosomal large ch
150	31	62.0	388	2	S26964	flavohemoglobin -
151	31	62.0	399	1	A26916	ribonucleoside-dip
152	31	62.0	429	2	AC1163	flagellar hook-ass
153	31	62.0	429	2	AC1522	flagellar hook-ass
154	31	62.0	442	2	T34661	hypothetical prote
155	31	62.0	465	2	T08290	hypothetical prote
156	31	62.0	466	2	AH1126	endo-1,4-beta-xyla
157	31	62.0	467	2	F64765	yaiU protein - Esc
158	31	62.0	475	2	A34443	nitrogen fixation
159	31	62.0	475	2	AG1995	nitrogen fixation
160	31	62.0	491	2	F87793	protein C27A12.6 [
161	31	62.0	521	1	VGIVDH	envelope glycoprot
162	31	62.0	544	2	S25101	CTP synthase (EC 6
163	31	62.0	572	2	T32523	hypothetical prote
164	31	62.0	579	2	B86565	oligopeptide perme
165	31	62.0	579	2	C72059	peptide ABC transp
166	31	62.0	596	2	D84972	ABC transporter AT
167	31	62.0	599	2	A48863	limonene cyclase -
168	31	62.0	601	2	A53318	malate dehydrogena
169	31	62.0	608	2	E71859	phosphogluconate d
170	31	62.0	619	2	F81532	conserved hypothet
171	31	62.0	619	2	E86617	CT858 hypothetical
172	31	62.0	619	2	F72006	CT858 hypothetical
173	31	62.0	623	2	A49112	sodium-glucose cot
174	31	62.0	632	2	T38617	probable ubiquitin
175	31	62.0	646	2	T33346	hypothetical prote
176	31	62.0	649	2	C32575	C-ski protein FB27
177	31	62.0	654	2	T33044	hypothetical prote
178	31	62.0	684	1	TVHUSN	transforming prote
179	31	62.0	690	2	I51298	transforming prote
180	31	62.0	713	2	B32575	C-ski protein FB28
181	31	62.0	717	1	S29923	transforming prote
182	31	62.0	727	1	A38206	procollagen-lysine
183	31	62.0	728	1	TVHUSK	transforming prote
184	31	62.0	728	2	S59964	procollagen-lysine
185	31	62.0	750	2	A32575	C-ski protein FB29
186	31	62.0	924	2	S06117	myosin heavy chain
187	31	62.0	930	2	T34334	hypothetical prote
188	31	62.0	961	2	AD0548	puative autotransp
189	31	62.0	971	2	A35697	transcription fact
190	31	62.0	980	2	H90681	probable flagellin
191	31	62.0	980	2	D85532	probable structura
192	31	62.0	1005	2	A64465	hypothetical prote
193	31	62.0	1053	2	T09645	DNA-directed RNA p
194	31	62.0	1191	2	B97116	chromosome segrega
195	31	62.0	1206	2	T44376	DNA-directed RNA p
196	31	62.0	1218	2	T29915	hypothetical prote
197	31	62.0	1227	2	B96673	hypothetical prote
198	31	62.0	1251	2	B86194	hypothetical prote
199	31	62.0	1265	2	T07397	kinesin heavy chai
200	31	62.0	1410	1	A57013	early endosome ant
201	31	62.0	1478	2	S78131	DNA-directed RNA p
202	31	62.0	1507	2	T42631	breast cancer tumo
203	31	62.0	1837	2	T41023	probable nuclear p
204	31	62.0	1976	2	A59252	myosin heavy chain
205	31	62.0	2007	1	B43402	myosin heavy chain
206	31	62.0	2606	2	T03159	large tegument pro
207	30	60.0	90	2	C64013	hypothetical prote
208	30	60.0	100	2	B87184	conserved hypothet
209	30	60.0	132	2	A96600	protein F14J16.12
210	30	60.0	134	2	A44173	calcitonin gene-re
211	30	60.0	142	2	A87653	CheE protein [impo
212	30	60.0	145	2	S62510	hypothetical prote
213	30	60.0	146	2	H69446	hypothetical prote
214	30	60.0	166	2	T39586	rna binding protei
215	30	60.0	174	2	T28844	hypothetical prote
216	30	60.0	196	2	D84178	50S ribosomal prot
217	30	60.0	203	2	T32346	hypothetical prote
218	30	60.0	206	1	E64327	H+-transporting tw
219	30	60.0	208	2	AB1706	hypothetical prote
220	30	60.0	212	1	A49436	dual specificity p
221	30	60.0	219	2	I52911	cytoskeletal prote
222	30	60.0	219	2	C91117	probable 2-compone
223	30	60.0	219	2	T02114	hypothetical prote
224	30	60.0	231	2	S73469	probable lipoprote
225	30	60.0	233	2	H86593	Yop translocation
226	30	60.0	233	2	D72030	type III secretion
227	30	60.0	241	2	I51211	cytoskeletal prote
228	30	60.0	241	2	S49014	lysin - Lactococcu
229	30	60.0	250	2	T13459	hypothetical prote
230	30	60.0	257	2	AB1208	extragenic suppres
231	30	60.0	257	2	AE1564	extragenic suppres
232	30	60.0	263	2	AB0209	IclR-family transc
233	30	60.0	265	1	E69864	myo-inositol-1(or
234	30	60.0	278	1	B69025	conserved hypothet
235	30	60.0	278	2	T34810	translation elonga
236	30	60.0	281	2	T31510	hypothetical prote
237	30	60.0	289	2	T48894	lipoprotein mtsA,
238	30	60.0	290	2	T40031	hypothetical prote
239	30	60.0	290	2	G97328	uncharacterized co
240	30	60.0	292	1	C64503	conserved hypothet
241	30	60.0	301	1	S19209	protein kinase (EC
242	30	60.0	303	2	A87616	hydrolase, carbon-
243	30	60.0	309	2	A43583	adhesin B precurso
244	30	60.0	310	2	T11551	adhesin - Streptoc
245	30	60.0	314	2	T23178	hypothetical prote
246	30	60.0	318	2	C71168	hypothetical prote
247	30	60.0	326	2	S50713	probable phosphoes
248	30	60.0	330	2	JC5935	exostose-related p

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 28, 2005, 18:56:43 ; Search time 38 Seconds
(without alignments)
17.452 Million cell updates/sec

Title: US-09-991-627-2
Perfect score: 50
Sequence: 1 NLEKETEGLR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	50	100.0	200	3	US-08-952-796-15	Sequence 15, Appl
2	50	100.0	243	4	US-09-079-030-119	Sequence 119, App
3	50	100.0	264	1	US-08-448-606-6	Sequence 6, Appli
4	50	100.0	267	1	US-07-959-946-3	Sequence 3, Appli
5	50	100.0	267	1	US-08-333-577-3	Sequence 3, Appli
6	50	100.0	267	3	US-08-952-796-2	Sequence 2, Appli
7	50	100.0	267	4	US-08-940-136-260	Sequence 260, App
8	50	100.0	267	4	US-09-919-039-27	Sequence 27, Appl
9	50	100.0	267	5	PCT-US92-08634-3	Sequence 3, Appli
10	35	70.0	100	4	US-09-513-999C-5033	Sequence 5033, Ap
11	35	70.0	188	4	US-10-000-489-60	Sequence 60, Appl
12	35	70.0	376	4	US-09-543-681A-6740	Sequence 6740, Ap
13	34	68.0	137	4	US-09-248-796A-14477	Sequence 14477, A
14	34	68.0	197	4	US-09-107-532A-4134	Sequence 4134, Ap
15	34	68.0	422	2	US-09-067-351-3	Sequence 3, Appli
16	34	68.0	422	3	US-09-360-490-3	Sequence 3, Appli
17	34	68.0	470	4	US-09-886-319A-35	Sequence 35, Appl
18	34	68.0	475	4	US-09-107-532A-3866	Sequence 3866, Ap
19	34	68.0	550	4	US-09-344-510B-4	Sequence 4, Appli
20	34	68.0	596	4	US-09-134-000C-4516	Sequence 4516, Ap
21	34	68.0	1014	4	US-09-344-510B-3	Sequence 3, Appli
22	34	68.0	1195	4	US-09-538-092-517	Sequence 517, App
23	33	66.0	235	3	US-09-134-001C-5145	Sequence 5145, Ap
24	33	66.0	249	4	US-09-107-532A-4520	Sequence 4520, Ap
25	33	66.0	432	4	US-09-917-254-80	Sequence 80, Appl
26	33	66.0	519	4	US-09-134-000C-4482	Sequence 4482, Ap
27	32	64.0	54	1	US-08-346-849-13	Sequence 13, Appl
28	32	64.0	54	2	US-08-293-284A-13	Sequence 13, Appl
29	32	64.0	54	4	US-08-898-300-13	Sequence 13, Appl
30	32	64.0	109	4	US-09-248-796A-22489	Sequence 22489, A
31	32	64.0	310	1	US-07-791-377-2	Sequence 2, Appli
32	32	64.0	310	3	US-08-356-106-2	Sequence 2, Appli
33	32	64.0	356	4	US-09-489-039A-10259	Sequence 10259, A
34	32	64.0	396	3	US-08-985-908-24	Sequence 24, Appl
35	32	64.0	402	4	US-09-489-039A-12073	Sequence 12073, A
36	32	64.0	606	4	US-09-460-295B-12	Sequence 12, Appl
37	32	64.0	623	4	US-09-252-991A-31173	Sequence 31173, A
38	32	64.0	721	4	US-09-248-796A-18800	Sequence 18800, A
39	32	64.0	982	4	US-09-023-905A-7	Sequence 7, Appli
40	32	64.0	998	4	US-09-198-452A-841	Sequence 841, App
41	32	64.0	2871	4	US-09-538-092-936	Sequence 936, App
42	31	62.0	21	2	US-08-846-526-1	Sequence 1, Appli
43	31	62.0	70	4	US-09-450-209-2	Sequence 2, Appli
44	31	62.0	75	1	US-08-422-613-4	Sequence 4, Appli
45	31	62.0	86	4	US-09-513-999C-5451	Sequence 5451, Ap
46	31	62.0	92	4	US-09-328-352-4270	Sequence 4270, Ap
47	31	62.0	95	4	US-09-270-767-39763	Sequence 39763, A
48	31	62.0	95	4	US-09-270-767-54980	Sequence 54980, A
49	31	62.0	102	1	US-08-409-373B-2	Sequence 2, Appli
50	31	62.0	102	1	US-08-409-373B-2	Sequence 2, Appli
51	31	62.0	102	3	US-08-621-018B-2	Sequence 2, Appli
52	31	62.0	102	4	US-09-483-665-2	Sequence 2, Appli
53	31	62.0	124	4	US-09-621-976-4246	Sequence 4246, Ap
54	31	62.0	128	4	US-09-513-999C-5082	Sequence 5082, Ap
55	31	62.0	156	4	US-09-252-991A-16963	Sequence 16963, A
56	31	62.0	200	4	US-09-248-796A-25873	Sequence 25873, A
57	31	62.0	235	4	US-09-198-452A-930	Sequence 930, App
58	31	62.0	241	2	US-08-379-556A-4	Sequence 4, Appli
59	31	62.0	286	1	US-08-358-117-2	Sequence 2, Appli
60	31	62.0	286	1	US-08-872-784-3	Sequence 3, Appli
61	31	62.0	286	2	US-09-100-851-3	Sequence 3, Appli
62	31	62.0	286	3	US-09-265-294-3	Sequence 3, Appli
63	31	62.0	378	4	US-09-248-796A-14749	Sequence 14749, A
64	31	62.0	460	4	US-09-198-452A-638	Sequence 638, App
65	31	62.0	467	4	US-09-492-709A-381	Sequence 381, App
66	31	62.0	599	2	US-08-846-526-11	Sequence 11, Appl
67	31	62.0	599	3	US-09-172-339-2	Sequence 2, Appli
68	31	62.0	599	4	US-09-398-395A-22	Sequence 22, Appl
69	31	62.0	599	4	US-09-887-586A-22	Sequence 22, Appl
70	31	62.0	599	4	US-09-895-752-22	Sequence 22, Appl
71	31	62.0	599	4	US-09-903-012B-22	Sequence 22, Appl
72	31	62.0	599	4	US-09-900-797-22	Sequence 22, Appl
73	31	62.0	624	4	US-09-198-452A-1089	Sequence 1089, Ap
74	31	62.0	727	3	US-08-989-385-4	Sequence 4, Appli
75	31	62.0	727	4	US-09-593-826-4	Sequence 4, Appli
76	31	62.0	750	3	US-08-202-841A-2	Sequence 2, Appli
77	31	62.0	1263	3	US-09-351-224E-11	Sequence 11, Appl
78	31	62.0	1263	4	US-09-677-488A-11	Sequence 11, Appl
79	31	62.0	1263	4	US-09-677-682B-11	Sequence 11, Appl
80	31	62.0	1494	3	US-08-755-587-186	Sequence 186, App
81	31	62.0	1761	4	US-09-561-709B-1	Sequence 1, Appli
82	31	62.0	1976	4	US-09-538-092-1078	Sequence 1078, Ap
83	30	60.0	82	4	US-09-513-999C-7488	Sequence 7488, Ap
84	30	60.0	96	4	US-09-513-999C-5243	Sequence 5243, Ap
85	30	60.0	115	4	US-09-513-999C-7866	Sequence 7866, Ap
86	30	60.0	133	4	US-09-513-999C-5244	Sequence 5244, Ap
87	30	60.0	137	4	US-09-134-000C-5507	Sequence 5507, Ap
88	30	60.0	140	4	US-09-198-452A-888	Sequence 888, App
89	30	60.0	146	1	US-08-688-609-6	Sequence 6, Appli
90	30	60.0	146	3	US-09-002-832-6	Sequence 6, Appli
91	30	60.0	146	4	US-09-976-594-830	Sequence 830, App
92	30	60.0	147	1	US-08-688-609-8	Sequence 8, Appli
93	30	60.0	147	3	US-09-002-832-8	Sequence 8, Appli
94	30	60.0	148	1	US-08-688-609-3	Sequence 3, Appli
95	30	60.0	148	3	US-09-002-832-3	Sequence 3, Appli
96	30	60.0	150	4	US-09-621-976-4203	Sequence 4203, Ap
97	30	60.0	152	4	US-08-311-731A-272	Sequence 272, App
98	30	60.0	153	4	US-09-270-767-35615	Sequence 35615, A
99	30	60.0	153	4	US-09-270-767-50832	Sequence 50832, A
100	30	60.0	173	4	US-09-270-767-44378	Sequence 44378, A

101	30	60.0	189	4	US-09-270-767-37522	Sequence 37522, A
102	30	60.0	189	4	US-09-270-767-52739	Sequence 52739, A
103	30	60.0	212	1	US-08-461-859-35	Sequence 35, Appl
104	30	60.0	212	4	US-09-917-254-62	Sequence 62, Appl
105	30	60.0	216	4	US-09-198-452A-627	Sequence 627, App
106	30	60.0	249	3	US-08-952-127-19	Sequence 19, Appl
107	30	60.0	254	4	US-09-270-767-44283	Sequence 44283, A
108	30	60.0	302	4	US-09-134-000C-6572	Sequence 6572, Ap
109	30	60.0	336	4	US-09-673-395A-600	Sequence 600, App
110	30	60.0	341	4	US-09-538-092-305	Sequence 305, App
111	30	60.0	345	4	US-09-538-092-194	Sequence 194, App
112	30	60.0	355	4	US-09-248-796A-18246	Sequence 18246, A
113	30	60.0	374	4	US-09-252-991A-27773	Sequence 27773, A
114	30	60.0	382	2	US-08-477-451-28	Sequence 28, Appl
115	30	60.0	396	4	US-09-800-729-207	Sequence 207, App
116	30	60.0	397	4	US-09-079-030-123	Sequence 123, App
117	30	60.0	432	4	US-09-792-024-104	Sequence 104, App
118	30	60.0	447	4	US-09-248-796A-14846	Sequence 14846, A
119	30	60.0	453	4	US-09-583-110-4631	Sequence 4631, Ap
120	30	60.0	481	4	US-09-252-991A-31018	Sequence 31018, A
121	30	60.0	519	3	US-08-997-445D-2	Sequence 2, Appli
122	30	60.0	650	1	US-08-224-657-97	Sequence 97, Appl
123	30	60.0	650	3	US-09-354-138-97	Sequence 97, Appl
124	30	60.0	662	1	US-08-224-657-94	Sequence 94, Appl
125	30	60.0	662	3	US-09-354-138-94	Sequence 94, Appl
126	30	60.0	681	4	US-09-248-796A-17026	Sequence 17026, A
127	30	60.0	785	4	US-09-134-000C-6690	Sequence 6690, Ap
128	30	60.0	816	4	US-10-101-464A-827	Sequence 827, App
129	30	60.0	867	2	US-08-938-365-2	Sequence 2, Appli
130	30	60.0	954	2	US-08-749-169A-3	Sequence 3, Appli
131	30	60.0	954	2	US-09-130-032A-3	Sequence 3, Appli
132	30	60.0	954	4	US-09-866-028-7	Sequence 7, Appli
133	30	60.0	954	4	US-09-944-457-7	Sequence 7, Appli
134	30	60.0	955	4	US-09-798-051-8	Sequence 8, Appli
135	30	60.0	1068	3	US-09-085-199B-11	Sequence 11, Appl
136	30	60.0	1240	4	US-10-101-464A-976	Sequence 976, App
137	30	60.0	1288	4	US-09-919-039-209	Sequence 209, App
138	30	60.0	1781	2	US-08-477-451-11	Sequence 11, Appl
139	30	60.0	1972	4	US-08-875-435B-3	Sequence 3, Appli
140	30	60.0	3056	1	US-08-508-836A-8	Sequence 8, Appli
141	30	60.0	3056	2	US-08-629-001A-3	Sequence 3, Appli
142	30	60.0	3056	2	US-08-874-266-2	Sequence 2, Appli
143	30	60.0	3056	3	US-08-642-274D-3	Sequence 3, Appli
144	30	60.0	3056	3	US-08-952-127-3	Sequence 3, Appli
145	30	60.0	3056	3	US-08-952-014C-3	Sequence 3, Appli
146	30	60.0	3056	4	US-09-360-416-2	Sequence 2, Appli
147	30	60.0	3056	4	US-08-984-090-2	Sequence 2, Appli
148	30	60.0	3057	4	US-09-360-416-3	Sequence 3, Appli
149	30	60.0	3666	2	US-08-222-617A-12	Sequence 12, Appl
150	30	60.0	3727	2	US-08-222-617A-27	Sequence 27, Appl
151	30	60.0	3778	2	US-08-222-617A-2	Sequence 2, Appli
152	29	58.0	35	2	US-08-491-527A-1	Sequence 1, Appli
153	29	58.0	35	2	US-08-845-659-1	Sequence 1, Appli
154	29	58.0	35	3	US-08-845-658-1	Sequence 1, Appli
155	29	58.0	35	3	US-09-518-178-1	Sequence 1, Appli
156	29	58.0	35	4	US-09-517-597-1	Sequence 1, Appli
157	29	58.0	57	3	US-09-015-030-11	Sequence 11, Appl
158	29	58.0	62	4	US-09-513-999C-7101	Sequence 7101, Ap
159	29	58.0	74	3	US-09-134-001C-5666	Sequence 5666, Ap
160	29	58.0	80	4	US-09-513-999C-6128	Sequence 6128, Ap
161	29	58.0	89	4	US-09-134-000C-6216	Sequence 6216, Ap
162	29	58.0	92	4	US-09-248-796A-24089	Sequence 24089, A
163	29	58.0	114	4	US-09-513-999C-5016	Sequence 5016, Ap
164	29	58.0	121	2	US-08-658-639-13	Sequence 13, Appl
165	29	58.0	121	3	US-08-944-604-13	Sequence 13, Appl
166	29	58.0	121	4	US-09-248-796A-22471	Sequence 22471, A
167	29	58.0	121	4	US-09-248-796A-26597	Sequence 26597, A
168	29	58.0	126	4	US-09-107-532A-4794	Sequence 4794, Ap
169	29	58.0	129	4	US-09-134-000C-6748	Sequence 6748, Ap
170	29	58.0	129	4	US-09-583-110-4161	Sequence 4161, Ap
171	29	58.0	134	4	US-09-270-767-31690	Sequence 31690, A
172	29	58.0	134	4	US-09-270-767-46907	Sequence 46907, A
173	29	58.0	141	2	US-08-658-639-14	Sequence 14, Appl
174	29	58.0	141	3	US-08-944-604-14	Sequence 14, Appl
175	29	58.0	160	4	US-09-489-039A-13473	Sequence 13473, A
176	29	58.0	162	4	US-09-489-039A-7850	Sequence 7850, Ap
177	29	58.0	170	3	US-08-858-207A-519	Sequence 519, App
178	29	58.0	171	4	US-09-248-796A-19229	Sequence 19229, A
179	29	58.0	175	4	US-09-252-991A-20191	Sequence 20191, A
180	29	58.0	208	4	US-09-107-532A-6124	Sequence 6124, Ap
181	29	58.0	211	4	US-09-543-681A-7263	Sequence 7263, Ap
182	29	58.0	226	4	US-09-248-796A-14924	Sequence 14924, A
183	29	58.0	228	4	US-09-252-991A-18371	Sequence 18371, A
184	29	58.0	228	4	US-09-543-681A-5765	Sequence 5765, Ap
185	29	58.0	242	3	US-08-977-865-4	Sequence 4, Appli
186	29	58.0	259	4	US-09-540-236-2575	Sequence 2575, Ap
187	29	58.0	263	4	US-09-583-110-3014	Sequence 3014, Ap
188	29	58.0	289	3	US-08-961-083-20	Sequence 20, Appl
189	29	58.0	289	4	US-09-536-784-20	Sequence 20, Appl
190	29	58.0	291	3	US-09-443-184-54	Sequence 54, Appl
191	29	58.0	293	4	US-09-071-035-496	Sequence 496, App
192	29	58.0	294	4	US-09-103-664A-5	Sequence 5, Appli
193	29	58.0	309	2	US-08-715-131-2	Sequence 2, Appli
194	29	58.0	309	3	US-09-221-753-2	Sequence 2, Appli
195	29	58.0	309	4	US-09-583-110-3218	Sequence 3218, Ap
196	29	58.0	309	4	US-09-754-809-2	Sequence 2, Appli
197	29	58.0	313	4	US-09-543-681A-5250	Sequence 5250, Ap
198	29	58.0	314	4	US-09-252-991A-24843	Sequence 24843, A
199	29	58.0	316	4	US-09-071-035-494	Sequence 494, App
200	29	58.0	317	4	US-09-583-110-4111	Sequence 4111, Ap
201	29	58.0	318	4	US-08-555-755C-6	Sequence 6, Appli
202	29	58.0	333	4	US-09-107-532A-4544	Sequence 4544, Ap
203	29	58.0	347	4	US-09-543-681A-5961	Sequence 5961, Ap
204	29	58.0	368	2	US-08-869-137-2	Sequence 2, Appli
205	29	58.0	370	4	US-09-270-767-46593	Sequence 46593, A
206	29	58.0	383	1	US-08-464-523B-31	Sequence 31, Appl
207	29	58.0	390	3	US-08-977-865-2	Sequence 2, Appli
208	29	58.0	401	4	US-09-491-577-56	Sequence 56, Appl
209	29	58.0	407	2	US-08-934-846-4	Sequence 4, Appli
210	29	58.0	407	3	US-09-238-557-4	Sequence 4, Appli
211	29	58.0	414	4	US-08-836-687B-32	Sequence 32, Appl
212	29	58.0	418	2	US-08-934-846-2	Sequence 2, Appli
213	29	58.0	418	3	US-09-238-557-2	Sequence 2, Appli
214	29	58.0	442	3	US-09-032-365A-17	Sequence 17, Appl
215	29	58.0	454	4	US-09-198-452A-197	Sequence 197, App
216	29	58.0	491	3	US-08-812-824-1	Sequence 1, Appli
217	29	58.0	502	4	US-09-540-236-3780	Sequence 3780, Ap
218	29	58.0	516	4	US-09-107-532A-7034	Sequence 7034, Ap
219	29	58.0	534	4	US-09-103-664A-2	Sequence 2, Appli
220	29	58.0	568	3	US-09-134-001C-3768	Sequence 3768, Ap
221	29	58.0	590	4	US-09-248-796A-14494	Sequence 14494, A
222	29	58.0	593	1	US-07-961-522-4	Sequence 4, Appli
223	29	58.0	593	1	US-08-217-438-4	Sequence 4, Appli
224	29	58.0	593	1	US-08-217-438-5	Sequence 5, Appli
225	29	58.0	593	1	US-08-487-890A-100	Sequence 100, App
226	29	58.0	593	1	US-08-321-978-4	Sequence 4, Appli
227	29	58.0	593	2	US-08-710-584-4	Sequence 4, Appli
228	29	58.0	593	2	US-08-478-435-100	Sequence 100, App
229	29	58.0	593	2	US-08-337-483-100	Sequence 100, App
230	29	58.0	593	2	US-08-478-373-100	Sequence 100, App
231	29	58.0	593	3	US-08-474-671-100	Sequence 100, App
232	29	58.0	593	3	US-08-483-577A-100	Sequence 100, App
233	29	58.0	593	3	US-08-897-438-100	Sequence 100, App
234	29	58.0	593	3	US-08-637-654-100	Sequence 100, App
235	29	58.0	593	3	US-08-649-518-100	Sequence 100, App
236	29	58.0	593	4	US-08-753-750B-14	Sequence 14, Appl
237	29	58.0	620	4	US-09-538-092-1285	Sequence 1285, Ap
238	29	58.0	637	4	US-09-817-310-2	Sequence 2, Appli
239	29	58.0	662	3	US-09-061-768A-25	Sequence 25, Appl
240	29	58.0	662	4	US-09-764-246-25	Sequence 25, Appl
241	29	58.0	712	1	US-08-121-713D-64	Sequence 64, Appl
242	29	58.0	712	1	US-08-835-268-64	Sequence 64, Appl
243	29	58.0	712	2	US-09-060-692-64	Sequence 64, Appl
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245	29	58.0	712	3	US-09-060-610-64	Sequence 64, Appl
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